

SUPPLEMENTAL INFORMATION TO APPEAR ONLINE

Germ-free mice exhibit profound gut microbiota-dependent alterations of intestinal endocannabinoidome signaling

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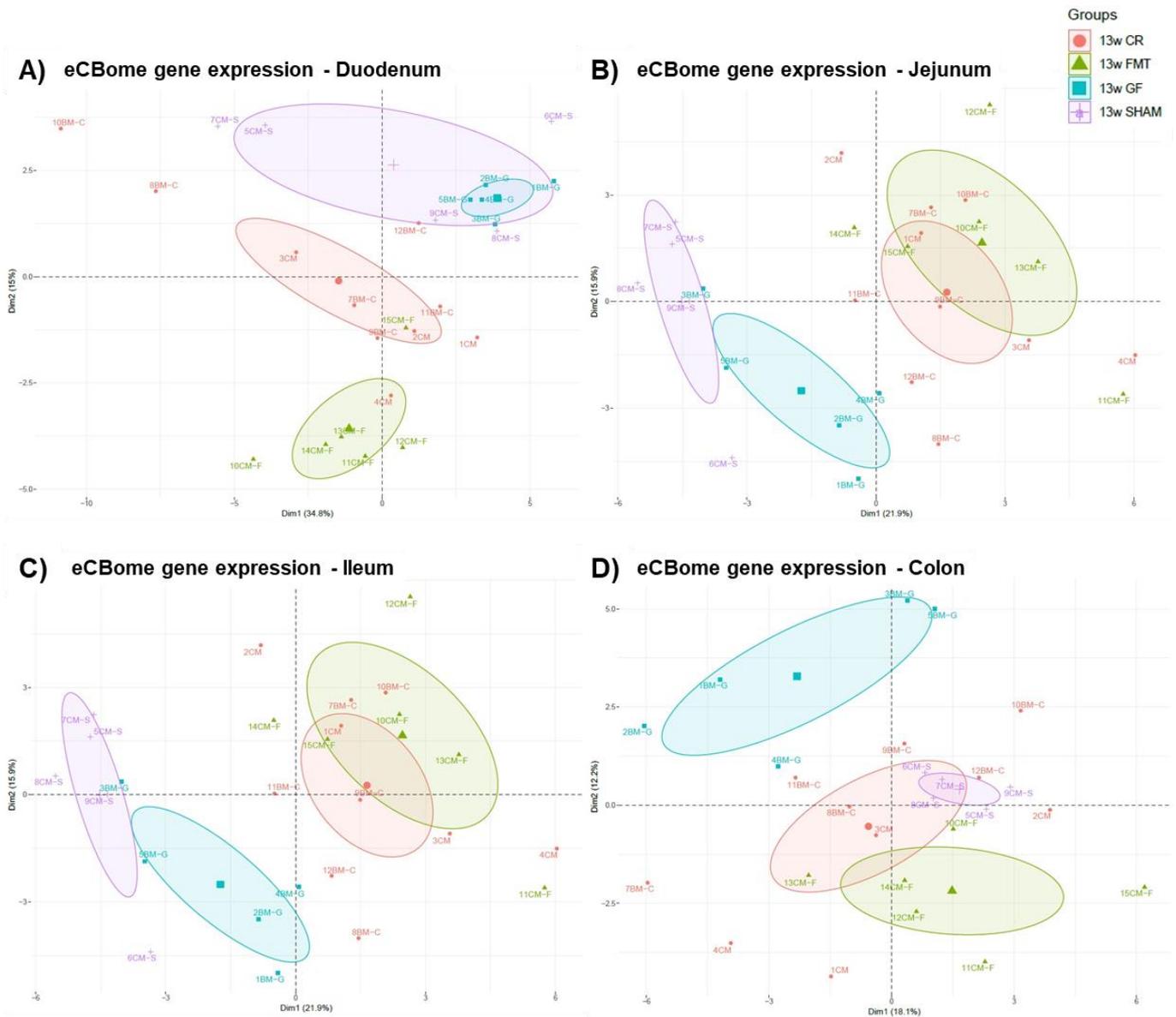
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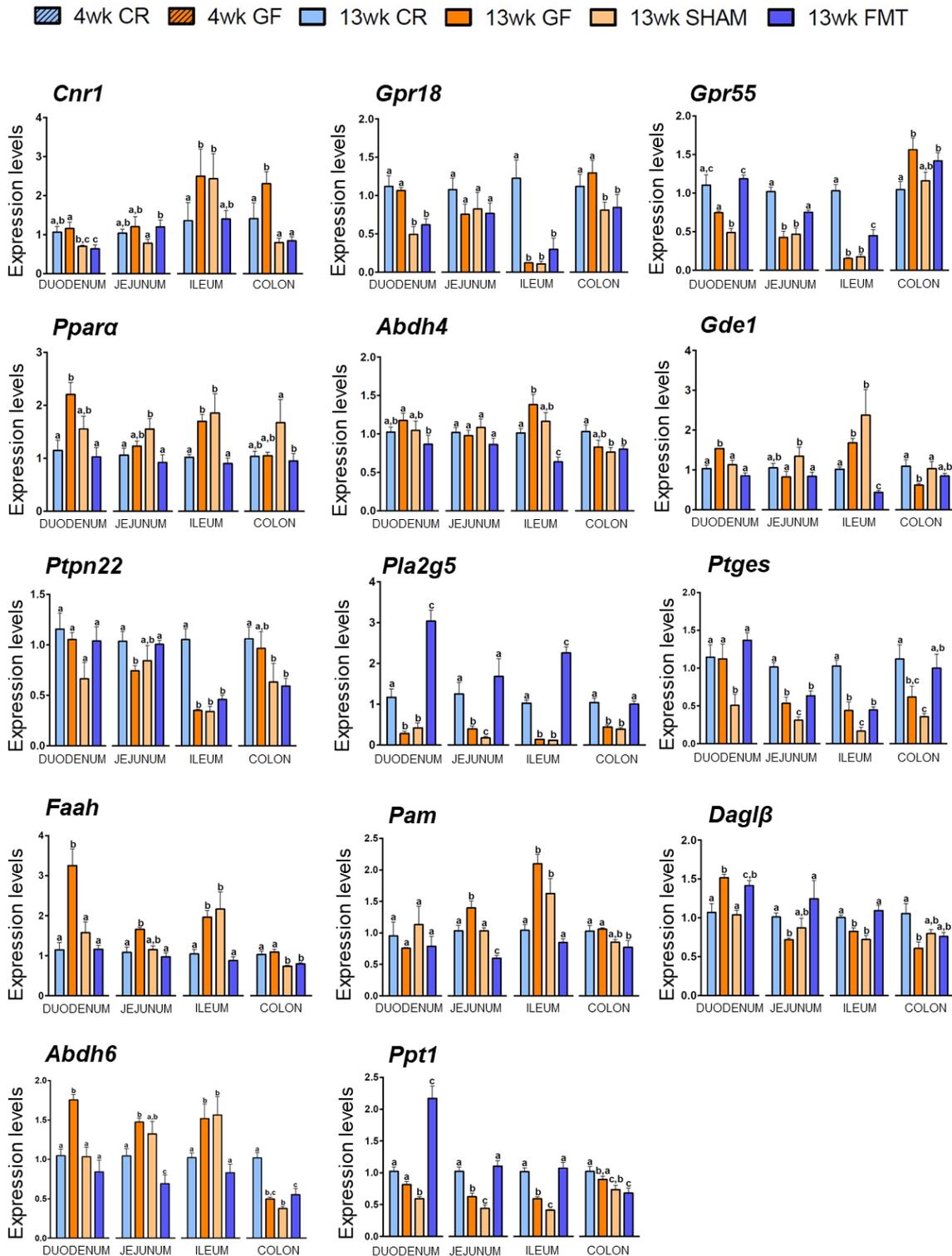
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Suppl. Fig. S1: Principal component analysis (PCA) showing that the reintroduction of the intestinal microbiota was able to partially reverse the gene expression changes observed in 13wk old GF mice particularly in A) duodenum, B) jejunum and C) ileum. In D) colon, FMT did not appear to bring overall gene expression back to that of GF mice and even GF and SHAM mice do not cluster together. CR: conventionally reared; FMT: Fecal Microbiota Transplanted mice, GF: Germ Free mice, SHAM: mice gavaged with sterile PBS.



Suppl. Fig. S2: The mRNA expression validations were determined, for 14 selected genes, in 13wk old GF, SHAM and FMT male mice in duodenum, jejunum, ileum and colon. Gene expression is reported as relative expression changes relative to age-matched CR. CR: conventionally reared; GF: Germ Free mice; SHAM: mice gavaged with sterile PBS; FMT: Fecal Microbiota Transplanted mice



Suppl. Table S1: List of the genes analyzed by qPCR array

Gene symbol	Gene name	Function
<i>Adgrf1</i>	adhesion G protein coupled receptor F1	receptor
<i>Cacna1b</i>	calcium channel, voltage-dependent, T type, alpha 1B subunit	receptor
<i>Cacna1h</i>	calcium channel, voltage-dependent, T type, alpha 1H subunit	receptor
<i>Cnr1</i>	cannabinoid receptor 1	receptor
<i>Cnr2</i>	cannabinoid receptor 2	receptor
<i>Gpr119</i>	G protein-coupled receptor 119	receptor
<i>Gpr18</i>	G protein-coupled receptor 18	receptor
<i>Gpr55</i>	G protein-coupled receptor 55	receptor
<i>Ppara</i>	peroxisome proliferator activated receptor alpha	receptor
<i>Pparg</i>	peroxisome proliferator activated receptor gamma	receptor
<i>Ptgfr</i>	prostaglandin F receptor	receptor
<i>Trpa1</i>	transient receptor potential cation channel, subfamily A, member 1	ligand-activated channel
<i>Trpm8</i>	transient receptor potential cation channel, subfamily M, member 8	ligand-activated channel
<i>Trpv1</i>	transient receptor potential cation channel, subfamily V, member 1	ligand-activated channel
<i>Trpv2</i>	transient receptor potential cation channel, subfamily V, member 2	ligand-activated channel
<i>Trpv4</i>	transient receptor potential cation channel, subfamily V, member 4	ligand-activated channel
<i>Abhd4</i>	abhydrolase domain containing 4	anabolic enzyme for NAEs
<i>Akr1b3</i>	aldo-keto reductase family 1, member B3 (aldose reductase)	anabolic enzyme for prostamides, catabolic enzyme for AEA and 2-AG
<i>Fam213b</i>	family with sequence similarity 213, member B	anabolic enzyme for prostamides, catabolic enzyme for AEA and 2-AG
<i>Gde1</i>	glycerophosphodiester phosphodiesterase 1	anabolic enzyme for NAEs
<i>Gdpd1</i>	glycerophosphodiester phosphodiesterase domain containing 1	anabolic enzyme for NAEs
<i>Glyat13</i>	glycine-N-acyltransferase-like 3	anabolic enzyme for N-acyl-glycines
<i>Hrasls5</i>	HRAS-like suppressor family, member 5	anabolic enzyme for NAEs
<i>Inpp5d</i>	inositol polyphosphate-5-phosphatase D	anabolic enzyme for NAEs
<i>Napepld</i>	N-acyl phosphatidylethanolamine-specific phospholipase D-like enzyme	anabolic enzyme for NAEs
<i>Pla2g10</i>	phospholipase A2, group X	anabolic enzyme for NAEs
<i>Pla2g4e</i>	phospholipase A2, group IVE	calcium-dependent N-acyltransferase that generates NAE biosynthetic precursors
<i>Pla2g5</i>	phospholipase A2, group V	AA-releasing enzyme possibly involved in phospholipid remodeling and hence biosynthesis of eCB precursors
<i>Ptgs2</i>	prostaglandin-endoperoxide synthase 2	anabolic enzyme for prostamides, catabolic enzyme for AEA and 2-AG
<i>Ptpn22</i>	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	anabolic enzyme for AEA

<i>Ptges</i>	prostaglandin E synthase	anabolic enzyme for prostamides, catabolic enzyme for AEA and 2-AG
<i>Comt</i>	catechol-O-methyltransferase	catabolic enzyme for <i>N</i> -acyl-dopamines
<i>Faah</i>	fatty acid amide hydrolase	catabolic enzyme for NAEs, primary fatty acid amides, <i>N</i> -acyl-taurines and <i>N</i> -acyl-glycines
<i>Naaa</i>	<i>N</i> -acylethanolamine acid amidase	catabolic enzyme for saturated NAEs
<i>Pam</i>	peptidylglycine alpha-amidating monooxygenase	anabolic enzyme for primary fatty acid amides, catabolic enzyme for <i>N</i> -acyl-glycines
<i>Dagla</i>	diacylglycerol lipase, alpha	anabolic enzyme for 2-acylglycerols
<i>Daglb</i>	diacylglycerol lipase, beta	anabolic enzyme for 2-acylglycerols
<i>Dgke</i>	diacylglycerol kinase, epsilon	anabolic/catabolic enzyme for 2-acylglycerols
<i>Enpp2</i>	ectonucleotide pyrophosphatase/phosphodiesterase 2	autotaxin- a LysoPLD: produces LPA.
<i>Pla1a</i>	phospholipase A1 member A	anabolic enzyme for 2-acylglycerols
<i>Plcb1</i>	phospholipase C, beta 1	anabolic enzyme for 2-acylglycerols
<i>Abhd12</i>	abhydrolase domain containing 12	catabolic enzyme for monoacylglycerols
<i>Abhd16a</i>	abhydrolase domain containing 16	catabolic enzyme for monoacylglycerols
<i>Abhd6</i>	abhydrolase domain containing 6	catabolic enzyme for monoacylglycerols
<i>Agk</i>	acylglycerol kinase	catabolic enzyme for monoacylglycerols
<i>Alox12</i>	arachidonate 12-lipoxygenase	catabolic enzyme for AEA and 2-AG
<i>Alox15</i>	arachidonate 15-lipoxygenase	catabolic enzyme for AEA and 2-AG
<i>Ces1d</i>	carboxylesterase 1D	catabolic enzyme for monoacylglycerols
<i>Ces2h</i>	carboxylesterase 2H	catabolic enzyme for monoacylglycerols
<i>Mgll (Magl)</i>	monoglyceride lipase	catabolic enzyme for monoacylglycerols
<i>Mogat1</i>	monoacylglycerol O-acyltransferase 1	catabolic enzyme for monoacylglycerols
<i>Ppt1</i>	palmitoyl-protein thioesterase 1	catabolic enzyme for 2-AG
<i>Gapdh</i>	glyceraldehyde-3-phosphate dehydrogenase	reference gene
<i>Hprt</i>	hypoxanthine guanine phosphoribosyl transferase	reference gene
<i>Rps13</i>	ribosomal protein S13	reference gene
<i>Tbp</i>	TATA box binding protein	reference gene

Supplemental Table S2: Primers used for qPCR validations

Gene	Forward sequence (5' → 3')	Reverse sequence (5' → 3')	Accession no.
<i>Abdh4</i>	ATGGCTGATGATCTGGAGCAG	CGGGCCAGGAACTTGTTCT	NM_134076.2
<i>Abdh6</i>	CAATCCTGGCATTGTGCGT	ATGGTGTGCGTAGCGAACTT	NM_025341.3
<i>Cnr1</i>	GGGCACCTTCACGGTTCTG	GTGGAAGTCAACAAAGCTGTAGA	NM_007726.3
<i>Daglb</i>	GGGCAAGGCGGCTCAAGTGT	GCCTCACAGAAGCCACGCACA	NM_144915.3
<i>Faah</i>	ACTTGGACGTGGTGCTAACC	GCCTATACCCTTTTTCATGCC	NM_010173.4
<i>Gdel</i>	GCTGCGGTTCTTCAGCTTC	CTCCACACCTGTTGCTCCATT	NM_019580.4
<i>Gpr18</i>	GTGGTGTTTTACCCAAGCCTC	TGGTCAGGGTCATTACCCAGA	NM_182806.2
<i>Gpr55</i>	CTGGCAGTCCATATCCCCAC	GCACCAGCAGTAAATCGAAAACA	NM_001033290.2
<i>Pam</i>	CTGGGGTCACACCTAAAGAGT	ATGAGGGCATGTTGCATCCAA	NM_013626.3
<i>Pla2g5</i>	CCAGGGGGCTTGCTAGAAC	AGCACCAATCAGTGCCATCC	NM_001122954.1
<i>Ppara</i>	AGAGCCCCATCTGTCCTCTC	ACTGGTAGTCTGCAAAACCAAA	NM_011144.6
<i>Ppt1</i>	ATACCTGGGATTTACGTCCTGT	TGACACACCATGTTGACTTGG	NM_008917.3
<i>Ptges</i>	GGATGCGCTGAAACGTGGA	CAGGAATGAGTACACGAAGCC	NM_022415.3
<i>Ptpn22</i>	GGCAATCCACCAAGTACAAGG	CCCTGGGTAGCAATATAAGCCT	NM_008979.1

Supplemental Table S3: differences in Ct of 4 and 13wk old CR male and female mice in the different

GENE	DUODENUM		JEJUNUM		ILEUM		COLON	
	4wk	13wk	4wk	13wk	4wk	13wk	4wk	13wk
<i>Adgrf1</i>	28,3	27,6	29,0	29,3	30,3	30,4	25,9	26,5
<i>Cacna1b</i>	29,3	28,8	27,9	29,2	27,8	28,6	25,9	26,6
<i>Cacna1h</i>	26,8	26,7	26,6	26,3	26,6	25,9	25,9	26,3
<i>Cnr1</i>	27,9	28,5	27,1	27,7	27,0	27,4	25,7	27,1
<i>Cnr2</i>	28,7	29,3	27,8	29,8	27,7	26,0	27,8	28,0
<i>Gpr119</i>	29,1	29,0	27,3	27,6	27,0	27,2	26,4	26,4
<i>Gpr18</i>	25,5	25,7	25,4	25,2	26,5	24,5	29,5	29,2
<i>Gpr55</i>	24,5	24,3	24,2	23,8	25,6	24,3	27,8	27,9
<i>Ppara</i>	20,9	21,8	21,1	21,4	22,2	22,5	23,3	24,0
<i>Pparg</i>	NA	NA	NA	NA	NA	NA	NA	NA
<i>Ptgfr</i>	NA	NA	NA	NA	29,9	29,3	29,3	29,8
<i>Trpa1</i>	25,4	26,1	27,1	26,2	29,2	29,1	29,1	30,1
<i>Trpm8</i>	NA	NA	NA	NA	NA	NA	NA	NA
<i>Trpv1</i>	29,3	NA	NA	NA	NA	NA	29,0	29,3
<i>Trpv2</i>	27,8	27,7	27,1	27,2	27,2	25,7	27,1	27,6
<i>Trpv4</i>	28,1	27,7	26,9	27,2	27,4	27,2	28,2	27,8
<i>Abhd4</i>	20,0	20,4	20,6	20,4	21,3	21,4	21,4	21,8
<i>Akr1b3</i>	23,7	23,2	22,3	23,0	22,6	22,5	21,7	21,6
<i>Fam213b</i>	20,8	21,1	20,1	20,1	20,9	20,8	24,3	24,4
<i>Gde1</i>	18,7	19,3	20,3	19,2	21,9	21,6	20,0	20,3
<i>Gdpd1</i>	20,3	20,7	17,9	19,2	18,1	18,6	19,6	19,9
<i>Glyat13</i>	NA	NA	NA	NA	NA	NA	NA	NA
<i>Hras15</i>	NA	NA	NA	NA	NA	NA	28,3	29,9
<i>Inpp5d</i>	24,5	25,4	24,7	24,7	24,9	23,7	26,0	26,3
<i>Napepld</i>	24,3	24,5	24,2	24,9	24,4	24,4	24,0	24,2
<i>Pla2g10</i>	25,0	24,5	23,2	24,2	23,4	23,7	20,1	20,5
<i>Pla2g4e</i>	NA	NA	NA	NA	NA	NA	NA	NA
<i>Pla2g5</i>	27,3	24,8	23,0	24,7	22,7	23,4	23,9	22,9
<i>Ptgs2</i>	29,9	29,4	28,5	28,3	28,6	28,3	28,5	30,0
<i>Ptpn22</i>	24,2	24,8	23,8	23,8	24,5	23,7	28,6	28,9
<i>Ptges</i>	27,1	27,6	25,8	26,2	26,2	25,8	27,8	28,3
<i>Comt</i>	19,9	20,7	20,1	20,3	20,6	20,7	21,1	21,4
<i>Faah</i>	19,0	20,5	19,1	19,4	20,7	21,1	22,6	22,8
<i>Naaa</i>	22,1	22,8	21,4	21,8	22,9	23,1	23,0	23,2
<i>Pam</i>	22,7	22,5	21,5	21,9	22,0	22,0	19,1	19,4
<i>Dagla</i>	27,5	27,1	25,4	26,5	25,1	25,4	24,5	24,9
<i>Daglb</i>	22,5	23,2	21,9	22,4	22,5	22,7	23,2	23,5
<i>Dgke</i>	26,4	26,0	25,6	26,0	25,7	25,5	25,4	25,5
<i>Enpp2</i>	27,7	27,6	26,6	26,9	26,0	24,8	25,7	25,6
<i>Pla1a</i>	29,7	29,8	29,3	29,0	29,6	28,2	29,6	29,5
<i>Plcb1</i>	28,0	27,9	25,5	26,8	25,5	25,8	26,0	26,4
<i>Abhd12</i>	19,7	20,5	19,6	20,1	20,2	20,4	22,4	22,7
<i>Abhd16a</i>	20,9	22,2	21,1	21,9	22,0	22,1	21,4	21,8
<i>Abhd6</i>	19,1	20,1	19,5	20,1	20,3	20,9	21,4	22,2
<i>Agk</i>	27,7	27,6	27,1	27,5	27,7	27,6	27,6	27,8
<i>Alox12</i>	28,7	27,5	28,9	29,3	NA	NA	28,8	28,9
<i>Alox15</i>	27,4	28,8	27,4	28,1	29,0	29,0	27,5	27,5
<i>Ces1d</i>	25,1	24,7	27,0	24,7	27,4	24,9	23,4	23,6
<i>Ces2h</i>	27,0	27,6	29,3	29,2	30,0	NA	30,4	29,6
<i>Mgl1 (Mag1)</i>	25,8	25,6	24,0	24,5	24,5	24,0	23,8	24,9
<i>Mogat1</i>	28,1	24,6	NA	NA	29,0	30,5	NA	NA
<i>Ppt1</i>	20,9	21,8	20,6	21,5	21,1	21,3	21,6	22,2
<i>Gapdh</i>	13,6	13,9	14,4	14,5	15,2	15,2	15,1	15,4
<i>Hprt</i>	21,3	21,1	21,0	21,0	21,0	21,0	21,2	21,7
<i>Rps13</i>	19,1	18,2	17,7	17,9	18,1	18,1	18,4	18,6
<i>Tbp</i>	23,0	23,2	22,7	22,7	22,9	22,7	23,0	23,3

segments of the intestine.

Table S.4: List of the lipid mediators used as internal standard for LC/MS-MS analyses

Lipid mediators symbol	Lipid mediators name
2-AG	d5-Mono-arachidonoyl-glycerol 1(3) and 2 isomers
AA	d8-Arachidonic acid
AEA	d4-Anandamide
Arachidonoyl Glycine	d8- <i>N</i> -Arachidonoyl Glycine
Arachidonoyl Serotonin	<i>N</i> -Arachidonoyl Serotonin
DHA	d5-Docosahexaenoic acid
DHEA	d4- <i>N</i> -docosahexaenoyl-ethanolamine
DPA	d5-Docosapentaenoic acid
2-DPG (n-3)	d5-Mono-docosapentaenoyl-glycerol 1(3) and 2 isomers
EPA	d5-Eicosapentaenoic acid
2-EPG	d5-Mono-eicosapentaenoyl-glycerol 1(3) and 2 isomers
EPEA	d4- <i>N</i> -eicosapentaenoyl-ethanolamine
LEA	d4- <i>N</i> -linoleoyl-ethanolamine
2-LG	d5-Mono-linoleoyl-glycerol 1(3) and 2 isomers
<i>N</i> -Oleoyl-L-Serine	<i>N</i> -Oleoyl-L-Serine
2-OG	2-oleoyl-glycerol
Oleoyl Serotonin	d17- <i>N</i> -oleoyl-serotonin
OEA	d4- <i>N</i> -oleoyl-ethanolamine
PEA	d4- <i>N</i> -palmitoyl-ethanolamine
2-PG	Mono-palmitoyl-glycerol 1(3) and 2 isomers
PGE2	d4-Prostaglandin E2
PGE2-EA	d4-Prostaglandin E2 ethanolamide (prostamide E2)
PGE2-G	d5-Prostaglandin E2 glycerol
PGF2 α -EA	Prostaglandin F2 α ethanolamide (prostamide F2 α)
Stearoyl-EA	d3- <i>N</i> -stearoyl-ethanolamine

Suppl. Table 5: p values indicating changes between the levels of the mediators in different intestinal segments at both 4wk (A) and 13wk (B) old mice. Green and red highlighting indicates an increase or decrease in mediators levels, respectively; ns: not statistically significant.

A)

4wk old mice	Duod vs Jej	Duod vs Ileum	Duod vs Colon	Jej vs Ileum	Jej vs Colon	Ileum vs Colon
AA	** 0,0087	ns	ns	ns	** 0,0087	ns
AEA	ns	* 0,0216	ns	** 0,0087	ns	* 0,0152
OEA	ns	ns	ns	ns	ns	ns
LEA	ns	** 0,0022	ns	ns	ns	** 0,0043
EPEA	ns	ns	ns	ns	ns	ns
DHEA	** 0,0022	** 0,0022	ns	** 0,0022	ns	* 0,026
2-AG	ns	ns	* 0,0152	* 0,0152	** 0,0022	* 0,0152
2-OG	* 0,0152	ns	ns	ns	* 0,0152	* 0,026
2-LG	ns	ns	* 0,026	* 0,0152	** 0,0087	ns
2-EPG	ns	ns	** 0,0087	** 0,0022	** 0,0022	* 0,026
2-DHG	ns	ns	** 0,0022	** 0,0022	** 0,0022	** 0,0022

B)

13wk old mice	Duod vs Jej	Duod vs Ileum	Duod vs Colon	Jej vs Ileum	Jej vs Colon	Ileum vs Colon
AA	** 0,0029	** 0,0068	ns	ns	* 0,0147	* 0,0185
AEA	** 0,005	ns	ns	**** < 0,0001	** 0,0068	** 0,0068
OEA	ns	ns	* 0,0115	ns	* 0,0232	ns
LEA	ns	ns	ns	ns	ns	* 0,0232
EPEA	* 0,0115	ns	ns	* 0,0354	ns	ns
DHEA	ns	**** < 0,0001	* 0,0354	*** 0,0003	* 0,0115	**** < 0,0001
2-AG	ns	** 0,0015	** 0,0052	**** < 0,0001	** 0,0089	ns
2-OG	ns	ns	ns	ns	ns	ns
2-LG	ns	* 0,0431	ns	* 0,0185	ns	ns
2-EPG	ns	** 0,0021	* 0,0431	*** 0,0002	* 0,0185	ns
2-DHG	ns	** 0,0029	ns	*** 0,0001	ns	ns

Suppl. Table 6: relative expression levels of the 52 eCBome-related genes of 4 and 13wk old male and female mice in duodenum, jejunum, ileum and colon with respect to age and sex-matched controls. The statistical analysis compared 4 and 13wk old GF male and female mice with respect to their age and sex-matched controls, while SHAM and FMT statistical analysis is relative to the 13wk male GF group. In **bold** are highlight statistically significant gene expression changes ($p \leq 0.05$). Green and red highlighting indicates an increase or decrease in gene expression, respectively. GF: Germ Free; SHAM: mice gavaged with sterile PBS; FMT: Fecal Microbiota Transplanted mice.

GENE	DUODENUM				JEJUNUM				ILEUM				COLON			
	4wk	13wk			4wk	13wk			4wk	13wk			4wk	13wk		
	GF	GF	SHAM	FMT	GF	GF	SHAM	FMT	GF	GF	SHAM	FMT	GF	GF	SHAM	FMT
<i>Adgrf1</i>	0,73	0,59	1,33	1,92	0,88	0,37	0,74	1,82	1,10	NA	NA	NA	0,28	1,24	1,68	2,90
<i>Cacna1b</i>	0,73	0,39	1,82	0,64	0,72	1,62	1,79	1,56	0,79	1,55	1,81	0,89	1,07	1,19	1,06	1,03
<i>Cacna1h</i>	1,39	0,52	1,09	0,57	1,25	1,16	1,08	0,97	0,62	1,28	2,09	0,58	1,69	1,40	0,90	0,74
<i>Cnr1</i>	1,30	0,83	0,90	0,73	1,14	0,85	1,17	1,41	0,78	1,77	1,70	1,33	2,79	2,17	0,71	0,66
<i>Cnr2</i>	1,07	1,04	0,58	0,57	0,56	2,46	2,05	0,85	1,39	0,10	0,13	0,76	1,04	1,53	1,16	1,09
<i>Gpr119</i>	1,46	0,92	1,11	0,56	1,28	0,92	1,12	0,65	1,35	1,19	0,98	0,86	1,40	1,11	0,95	0,99
<i>Gpr18</i>	0,50	0,80	0,56	0,80	0,51	0,66	1,08	1,10	0,33	0,06	0,06	0,13	1,31	1,01	1,65	0,94
<i>Gpr55</i>	0,68	0,58	0,55	1,03	0,60	0,44	0,73	0,91	0,51	0,19	0,22	0,40	0,90	1,49	1,16	0,81
<i>Ppara</i>	1,88	1,96	1,51	0,99	2,56	1,23	1,56	1,00	1,70	1,71	2,01	1,13	1,33	1,14	1,26	1,02
<i>Pparg</i>	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>Ptgfr</i>	NA	NA	NA	NA	NA	NA	NA	NA	0,49	1,35	1,25	0,81	1,61	1,21	1,06	1,02
<i>Trpa1</i>	1,26	1,27	0,82	1,33	1,74	0,63	0,66	1,08	1,62	0,76	1,30	1,29	2,57	1,85	1,97	2,15
<i>Trpm8</i>	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>Trpv1</i>	0,85	NA	NA	NA	1,24	0,70	2,04	0,94	NA	NA	NA	NA	0,40	1,53	1,86	2,12
<i>Trpv2</i>	0,88	0,53	0,79	0,81	0,61	0,86	0,87	1,07	0,68	0,39	0,55	0,40	1,95	1,86	0,67	0,79
<i>Trpv4</i>	0,74	0,34	0,83	0,67	0,97	1,48	1,68	0,73	0,63	1,01	0,76	0,64	0,78	0,58	0,53	0,72
<i>Abhd4</i>	1,12	0,99	1,06	0,87	1,61	0,90	1,29	1,03	1,37	1,35	1,51	0,84	0,90	0,79	0,89	0,91
<i>Akr1b3</i>	0,95	0,51	0,85	1,12	0,72	0,97	0,83	1,23	0,82	0,71	0,80	0,95	0,78	0,80	1,07	1,16
<i>Fam213b</i>	1,19	1,52	1,45	1,02	1,09	0,99	1,76	1,15	1,30	1,01	1,53	0,96	0,74	0,72	1,16	0,98
<i>Gde1</i>	1,04	1,45	1,17	0,81	2,55	0,84	1,58	0,92	2,34	1,62	1,64	0,55	0,88	0,90	1,01	0,84
<i>Gdpd1</i>	1,17	1,22	1,05	1,25	0,68	1,37	1,25	0,94	0,75	0,80	0,81	1,28	1,02	1,07	0,86	0,78
<i>Glyat13</i>	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>Hrasls5</i>	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0,65	0,74	1,12	2,02
<i>Inpp5d</i>	0,71	1,28	0,62	0,91	0,89	1,02	0,79	0,57	0,83	0,30	0,21	0,35	1,07	1,13	0,61	0,79
<i>Napepld</i>	0,73	0,60	1,02	1,14	0,92	1,04	0,76	0,66	0,87	0,95	0,81	0,94	0,75	0,93	0,89	1,17
<i>Pla2g10</i>	1,06	0,42	1,93	0,53	0,73	0,78	1,03	0,96	0,61	0,70	0,72	0,91	0,64	0,89	1,11	1,10
<i>Pla2g4e</i>	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>Pla2g5</i>	1,01	0,22	0,45	2,91	0,08	0,38	0,25	2,16	0,08	0,16	0,15	2,56	0,40	0,55	0,49	1,34
<i>Ptgs2</i>	1,04	0,60	0,94	0,95	0,57	0,54	0,53	0,87	0,65	1,17	0,88	0,82	0,92	1,23	1,25	1,23
<i>Ptpn22</i>	0,59	1,14	0,75	1,17	0,65	0,80	1,00	1,05	0,44	0,28	0,35	0,62	0,81	1,86	1,25	1,23
<i>Ptges</i>	0,77	0,94	0,60	1,86	0,29	0,53	0,44	0,94	0,25	0,55	0,29	0,66	0,60	0,86	0,51	1,22
<i>Comt</i>	0,89	1,09	1,11	1,24	1,31	1,24	1,64	1,41	1,27	1,23	1,34	0,91	1,05	1,03	0,93	0,90
<i>Faah</i>	1,37	2,51	1,55	1,12	1,69	1,35	1,71	1,23	2,27	1,73	1,82	1,21	1,21	1,06	0,92	0,97
<i>Naaa</i>	1,35	1,39	1,24	0,93	1,67	1,57	2,06	1,37	1,63	1,27	1,23	0,99	0,67	1,12	1,28	0,97
<i>Pam</i>	1,52	0,70	1,06	0,77	1,23	1,46	1,40	0,85	1,41	1,72	1,82	0,99	0,75	1,07	1,15	1,04
<i>Dagla</i>	0,95	0,45	1,09	1,38	0,66	1,07	0,96	1,39	0,62	0,79	0,83	1,20	1,05	0,94	0,92	1,04
<i>Daglb</i>	1,01	1,31	1,21	1,56	0,85	0,74	0,85	0,93	0,68	0,78	0,93	1,30	1,08	0,69	0,69	1,08
<i>Dgke</i>	1,21	0,62	0,86	0,80	1,05	1,08	0,82	0,98	0,87	1,25	0,86	0,92	1,28	1,10	0,74	0,68
<i>Enpp2</i>	1,11	0,32	0,61	0,67	0,54	1,12	0,80	1,58	0,69	0,86	0,65	0,44	0,93	1,07	0,74	1,10
<i>Pla1a</i>	0,77	0,81	1,04	0,64	0,62	0,61	1,22	0,77	0,90	0,66	0,57	0,51	0,70	1,06	1,39	0,88
<i>Plcb1</i>	1,51	0,69	0,91	0,87	0,87	1,59	1,28	1,09	0,95	1,34	1,23	0,98	1,70	1,38	0,80	0,90
<i>Abhd12</i>	0,87	1,30	1,34	0,83	1,16	1,31	1,80	1,12	1,07	1,04	1,22	0,68	0,87	0,94	0,94	0,95
<i>Abhd16a</i>	0,86	1,49	0,87	0,72	1,25	1,18	0,96	0,36	0,95	0,88	1,28	0,97	1,09	1,32	1,16	1,08
<i>Abhd6</i>	1,04	1,32	1,33	0,91	1,42	1,38	1,79	0,94	1,19	1,55	1,93	1,03	0,79	0,51	0,58	0,89
<i>Agk</i>	1,26	0,74	0,77	0,75	0,98	0,95	0,95	0,62	0,84	0,73	0,68	1,27	0,79	0,97	0,99	1,27
<i>Alox12</i>	1,52	0,28	0,69	0,34	0,65	0,84	1,11	0,68	NA	NA	NA	NA	1,06	0,43	0,90	0,63
<i>Alox15</i>	0,73	0,99	0,88	1,26	0,54	0,67	0,61	0,76	0,22	0,78	0,96	0,95	0,48	1,94	1,06	0,84
<i>Ces1d</i>	3,62	1,83	1,76	0,62	2,07	1,35	1,97	0,98	1,45	2,53	2,09	0,58	1,29	0,75	0,67	0,98
<i>Ces2h</i>	0,74	0,73	0,85	0,55	1,05	0,64	0,83	1,18	0,86	NA	NA	NA	0,80	0,72	0,55	0,77
<i>Mgll (Magl)</i>	1,82	0,80	1,38	0,77	0,67	1,07	0,93	1,07	0,73	1,41	1,18	0,81	1,26	0,79	0,47	1,02
<i>Mogat1</i>	0,50	0,17	2,80	0,83	NA	NA	NA	NA	2,68	NA	NA	NA	NA	NA	NA	NA
<i>Ppt1</i>	0,56	0,71	0,69	2,52	0,49	0,59	0,58	1,78	0,70	0,74	0,51	1,10	0,94	1,14	0,80	0,83